

Crystal Structure of Arylesterase from *Vibrio Mimicus*

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Beamline(s): X4A

Introduction: Esterases (E.C. 3.1.1.) are widely distributed in nature and catalyze the hydrolysis of ester bonds. Arylesterases (E.C. 3.1.1.2.) show a preferential substrate specificity for aromatic esters. The mammalian arylesterases play important roles in the detoxification of organophosphorous compounds and are used as diagnostic indicators for liver cirrhosis. Very little is known about the genetics and biochemistry of bacterial arylesterases. No crystal structure of this kind of arylesterase is available. Hence the structure determination will not only provide structure information of this kind of arylesterases, but also illustrate the structure and function relationship and possible application to industry.

Methods and Materials: The structure was solved by ISIRAS method, Au atoms were located by shelx90, phase was refined by SHARP, manual graphic inspection by O and structure was refined by CNS and refmac.

Results: The tertiary fold of the enzyme is different from the α/β hydrolase fold found in most of neutral lipases and esterases and is similar to that of small GTPases. The unique Gly-Asp-Ser-Leu-Ser is located at a Ω -loop and the first serine was confirmed as a nucleophilic residue both by mutation study and complex structure of diethyl-p-nitrophenolphosphate (DNP). This active Ser10 is hydrogen bonded to His160, which in turn interacts with Asp157. These three residues form a catalytic triad of Ser10-His160-Asp157 that closely resembling other serine hydrolases. The sidechain of Asn76 and the mainchain of Asp9 and Gly47 are positioned to create an oxyanion hole. Leu11, Ala75, Leu79, Ile110, Val112, Phe124 and Phe142 residues form a hydrophobic substrate binding pocket. Two arylesterases form a weak dimer through the H-bonding between Gln16 from each monomer and there is no clear secondary structure elements that forms a "lid" like structure commonly found in neutral lipases.

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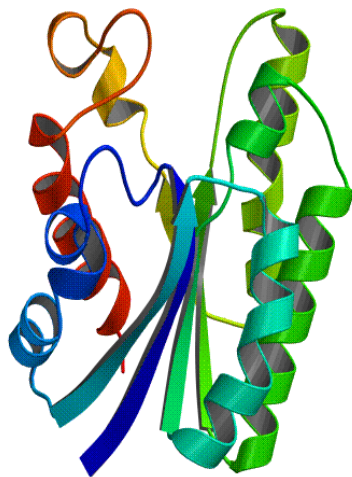


Figure 1. The ribbon drawing of arylesterase from *vibrio mimicus* shows a $\alpha/\beta/\alpha$ sandwich fold which is similar to that of the small GTPase protein.